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AUTHOR(S):

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## **$^1\text{H}$ , $^{13}\text{C}$ , and $^{15}\text{N}$ resonance assignment of the TIR domain of human MyD88**

Hidenori Ohnishi<sup>1</sup>, Hidehito Tochio<sup>2</sup>, Zenichiro Kato<sup>1</sup>, Takeshi Kimura<sup>1</sup>, Hidekazu

Hiroaki<sup>3</sup>, Naomi Kondo<sup>1</sup>, and Masahiro Shirakawa<sup>2</sup>

1. Department of Pediatrics, Graduate School of Medicine, Gifu University, Gifu,  
Japan

2. Department of Molecular Engineering, Graduate School of Engineering, Kyoto  
University, Kyoto, Japan.

3. Division of Structural Biology, Graduate School of Medicine, Kobe University,  
7-5-1, Kusunoki-cho, Chuo-ku, Kobe, Hyogo, 650-0017, Japan.

### **Corresponding author:**

Hidenori Ohnishi

Department of Pediatrics, Graduate School of Medicine, Gifu University

Yanagido 1-1, Gifu 501-1194, Japan

Phone: +81-58-230-6386

Fax: +81-58-230-6387

E-mail: [ohnishih@gifu-u.ac.jp](mailto:ohnishih@gifu-u.ac.jp)

Hidehito Tochio

Department of Molecular Engineering, Graduate School of Engineering

Kyoto University, Kyoto 615-8510, Japan

Phone: +81-75-383-2536

Fax: +81-75-383-2541

E-mail: [tochio@moleng.kyoto-u.ac.jp](mailto:tochio@moleng.kyoto-u.ac.jp)

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Innate immunity, Toll-like receptor, NMR, MyD88, TIR domain

### **Abstract**

Myeloid differentiating factor 88 (MyD88) is one of a critical adaptor molecule in the Toll-like receptor (TLR) signaling pathway. The TIR domain of MyD88 serves

as a protein-protein interaction module and interacts with other TIR-containing proteins such as Mal (MyD88 adaptor-like) and Toll-like receptor 4 to form signal initiation complexes. Here we report the  $^{15}\text{N}$ ,  $^{13}\text{C}$ , and  $^1\text{H}$  chemical shift assignments of the TIR domain of MyD88. The resonance assignments obtained in this work will contribute to the study of heteromeric TIR-TIR interactions between MyD88 and TIR-containing receptors or adaptors.

## Biological context

MyD88 is an essential and universal cytosolic adaptor protein in the signal transduction pathways mediated by members of the IL-1 family, including IL-18, and the Toll-like receptors (TLRs). It consists of an N-terminal death domain, a C-terminal Toll/Interleukin-1 receptor (TIR) domain (~150 amino acid residues), and a small linker segment between them. In innate immune responses, MyD88 plays pivotal roles in bridging between membraneous TLR and downstream kinases, such as the IL-1 receptor-associated kinases (IRAKs), in the cytosol (O'Neill and Bowie, 2007). For example, in the TLR4 pathway, the cytosolic TIR

domain of lipopolysaccharide (LPS)-stimulated TLR4 interacts with the TIR domain of MyD88 (MyD88-TIR). Concurrently, the death domain of MyD88 interacts with the death domain of IRAK4, activating the kinase. This initiates a phosphorylation cascade that eventually activates the transcription factors NF- $\kappa$ B (nuclear factor  $\kappa$ B) and AP-1 (activator protein 1) (Akira et al., 2006).

The TIR domains serve as protein-protein interaction modules, which are conserved in the intracellular region of TLRs and also in cytosolic adaptor proteins such as MyD88, Mal (MyD88 adaptor-like), TRIF (TIR domain-containing adaptor inducing IFN- $\beta$ ), TRAM (TRIF-related adaptor molecule), and SARM (sterile  $\alpha$  and HEAT Armadillo motifs). The crystal structures of TIR domains of some mammalian membranous receptors (TLR1, TLR2, TLR10, IL-1RAPL) and a bacterial protein (*Paracoccus denitrificans* TIR (PdTIR)) have been reported (Chan et al., 2009; Khan et al., 2004; Nyman et al., 2008; Tao et al., 2002; Xu et al., 2000), in some of which homomeric TIR interfaces were observed. However, the functional relevance of such interactions remains obscure, as the formation of

these homo-dimers of TIR domains had not been observed in solution (Khan et al., 2004; Nyman et al., 2008).

In our previous study, the isolated MyD88-TIR was shown to exist as a monomer, while full-length MyD88 forms a dimer in solution. The dimerization appears to be mediated via homomeric interactions within its death domain (Ohnishi et al., 2009). In that study, we performed NMR titration experiments using  $^{15}\text{N}$  MyD88-TIR and characterized a functionally relevant heteromeric TIR-TIR interaction with another TIR domain derived from Mal, which had been shown to enhance LPS-stimulated TLR4 signaling. Interestingly, no interaction has been observed between TLR4-TIR and MyD88-TIR, while Mal has been shown to directly bind TLR4-TIR. Thus, Mal seems to bridge between TLR4 and MyD88. These results exemplified the binding specificity among TIRs and its importance in forming correct signal initiation complexes (Ohnishi et al., 2009).

Here, we describe the NMR assignments of the TIR domain of MyD88. In IL-1R

and TLR signaling, the heteromeric TIR interactions of MyD88 play a central role in the above-mentioned formation of the TLR signalosome. The resonance assignments form a substantial contribution to the study of the heteromeric TIR-TIR interactions between MyD88 and TIR containing receptors or adaptors.

## Methods and Experiments

### Sample preparation

The portion of the human MyD88 gene encoding the TIR domain (amino acid residues 148-296) was cloned into the vector pGEX-5X-3 digested with restriction enzymes, ECOR1 and NotI (GE Healthcare). This vector was transformed into *E. coli* BL-21 (DE3) (Novagen). The transformed bacterial cells were cultured at 37°C until the OD<sub>600</sub> reached approximately 0.5. The cells were then induced with 1.0 mM IPTG and cultured for 16 hours at 25°C. For <sup>15</sup>N- or <sup>13</sup>C,<sup>15</sup>N-double-labeling, rich growth media containing stable isotope-enriched nutrients (Silantes) were used. Harvested bacterial cells were once frozen and thawed before the next lysis step. The cells were resuspended in lysis buffer

(20mM Tris, pH 8.0, 400mM KCl, 1mM EDTA, 10mM 2-mercaptoethanol and protease inhibitors) and disrupted by sonication on ice. The supernatant was loaded onto a glutathione Sepharose 4B FF (GE Healthcare) affinity chromatography column. Lysis buffer at 30x the bed volume of this resin was used for the washing step. GST fused MyD88-TIR protein was eluted with elution buffer (50mM Tris, pH 8.0, and 10mM 2-mercaptoethanol, and 10mM reduced glutathione). The GST-tag was cleaved by digestion with Factor Xa (1% of total protein volume) (Haematologic Technologies Inc.). Subsequently, the TIR domain was purified by gel filtration (Sephacryl S-100 HR 26/60 column, GE Healthcare) and cation-exchange chromatography (Mono-S column, GE Healthcare). The gel filtration running buffer was 20 mM potassium phosphate buffer (pH 6.0) containing 100mM KCl, 0.1 mM EDTA and 10 mM DTT. Using this purification protocol,  $^{15}\text{N}$ -labeled or  $^{13}\text{C}$ ,  $^{15}\text{N}$ -doubly-labeled TIR domain of MyD88 wild-type proteins was prepared. The yields of these proteins were approximately 1.0 mg from 1 L of rich growth media containing stable isotope-enriched nutrients. For preparing samples where selected amino acids



were not labeled, proteins were over-expressed by the same method described above with a slight modification. The bacterial cells were first cultured in LB media and collected 30 min before IPTG induction by centrifugation. The cells were resuspended and cultured in  $^{15}\text{N}$ -enriched M9 media containing unlabelled Gly, Ser and Cys, or Arg alone to a final composition of 100 mg/L for protein expression (The details of this protocol will be published elsewhere by Dr. H. Hiroaki). To improve the sample solubility and stability, the sample buffer was replaced by 20 mM potassium phosphate buffer (pH 6.0) containing 0.1 mM EDTA, 10 mM DTT, 50 mM deuterated L-arginine, and 50 mM deuterated L-glutamic acid. The final concentrations of the protein samples for typical NMR experiments were about 0.3 mM (Golovanov et al., 2004).

### **NMR spectroscopy**

All NMR spectra were recorded at 25°C on a Bruker DRX500 or Avance800 spectrometer equipped with a cryogenic probe. For assignment of backbone  $^1\text{H}$ ,  $^{13}\text{C}$ , and  $^{15}\text{N}$  resonances, HNCA, HN(CO)CA, HNCACB, CBCA(CO)NH and 3D

$^1\text{H}$ - $^{15}\text{N}$  NOESY-HSQC spectra were recorded. For side chain resonance assignment, 2D constant-time  $^1\text{H}$ - $^{13}\text{C}$  HSQC,  $^1\text{H}$ - $^{13}\text{C}$  NOESY-HSQC, HCCH-TOCSY, CC(CO)NNH and HCC(CO)NNH were recorded. All NMR data were processed using NMRPipe (Delaglio et al., 1995), and analyzed using Sparky (Goddard and Kneller, 1999).

### Assignments and data deposition

Employment of 50 mM L-arginine and L-glutamic acid in the sample buffer significantly improved the solubility of the sample by approximately three fold, resulting in significantly enhanced NMR signal intensities. Following a standard sequential assignment procedure, 88.6% of the  $^1\text{H}^{\text{N}}$ ,  $^{15}\text{N}$  resonances of backbone amide groups (124 out of the 140 non-Pro residues) were assigned (Fig. 1). In addition, 91.3% of  $\text{H}\alpha$  (136 out of 149 residues), 93.3% (139 out of 149 residues) of  $^{13}\text{C}^{\alpha}$ , and 91.3% (136 out of 149 residues) of  $^{13}\text{C}^{\beta}$  resonances were assigned. The sequential correlations of the backbone resonances of 195–200, 202, and 203 were missing. Those residues are involved in the BB-loop region in the

structure of MyD88-TIR. Relatively lower  $\{^1\text{H}\}$ - $^{15}\text{N}$  hetero NOE values of amide groups at the neighboring residues suggested that the region did not adopt a fixed conformation, but had some flexibility (Ohnishi et al., 2009). This might have caused NMR signal broadening at the BB-loop residues. Besides those above-mentioned residues, Thr-185, Asp-186, Tyr-187, and Arg-188 in the turn region were also missing, which could also be due to NMR signal broadening caused by local motions. Nevertheless, substantial numbers of side chain  $^1\text{H}$  and  $^{13}\text{C}$  atoms of those residues have been assigned on the basis of  $^{13}\text{C}$  edited NOESY and HCCH-TOCSY spectra. The assigned chemical shifts of the TIR domain of MyD88 have been deposited in the BMRB database under accession number 11078. The coordinates of the TIR domain of human MyD88 have been deposited at the Protein Data Bank under accession code 2z5v.

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## Figure Legend

Fig. 1  $^1\text{H}$ ,  $^{15}\text{N}$  HSQC spectrum of uniformly  $^{15}\text{N}$ -labeled TIR domain of human MyD88 in 20 mM potassium phosphate buffer (pH 6.0) containing 0.1 mM EDTA, 10 mM DTT, 50 mM deuterated L-arginine, and 50 mM deuterated L-glutamic acid recorded at 25°C.

